

FIG. 1

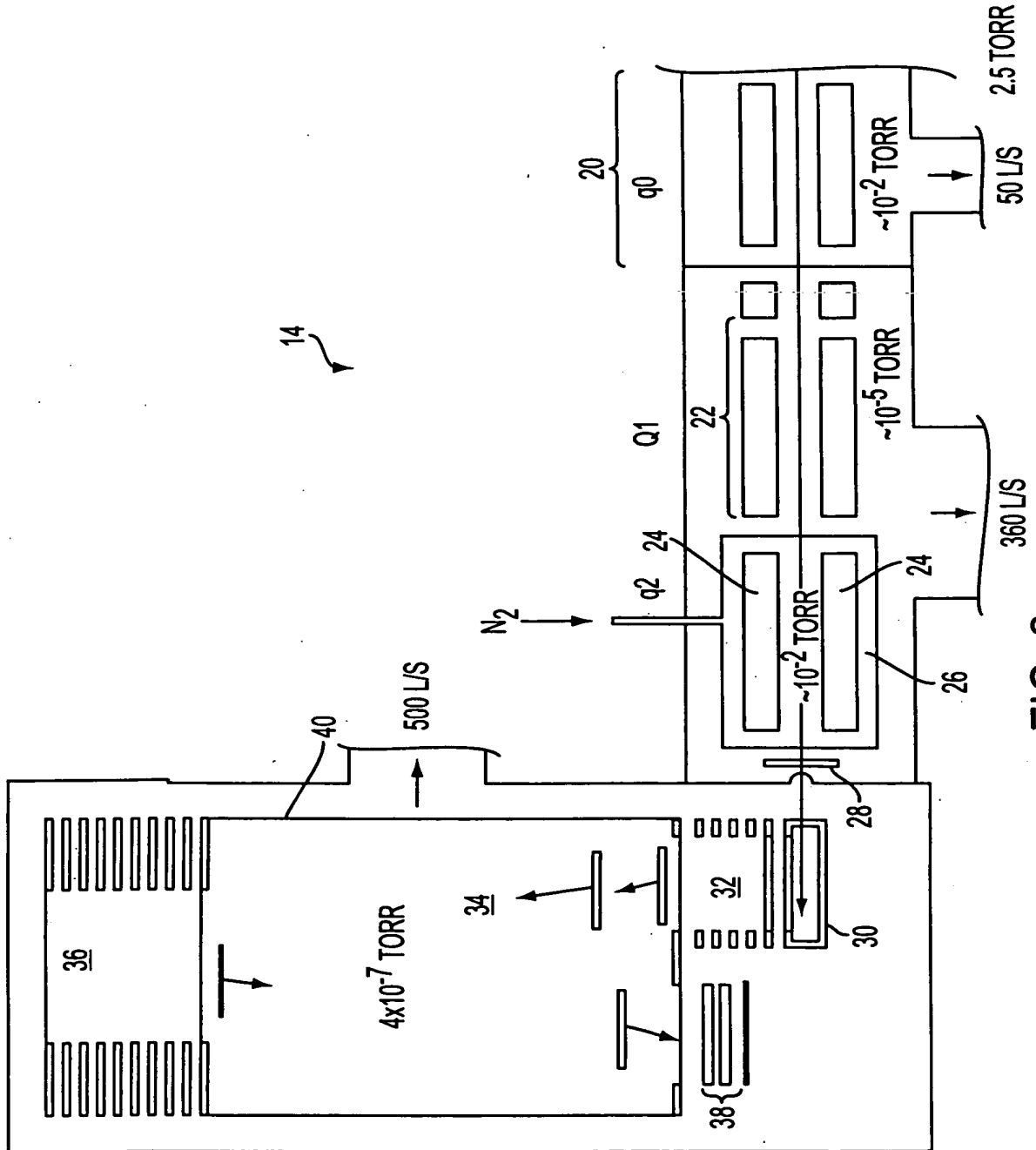


FIG. 2

201510-65599001

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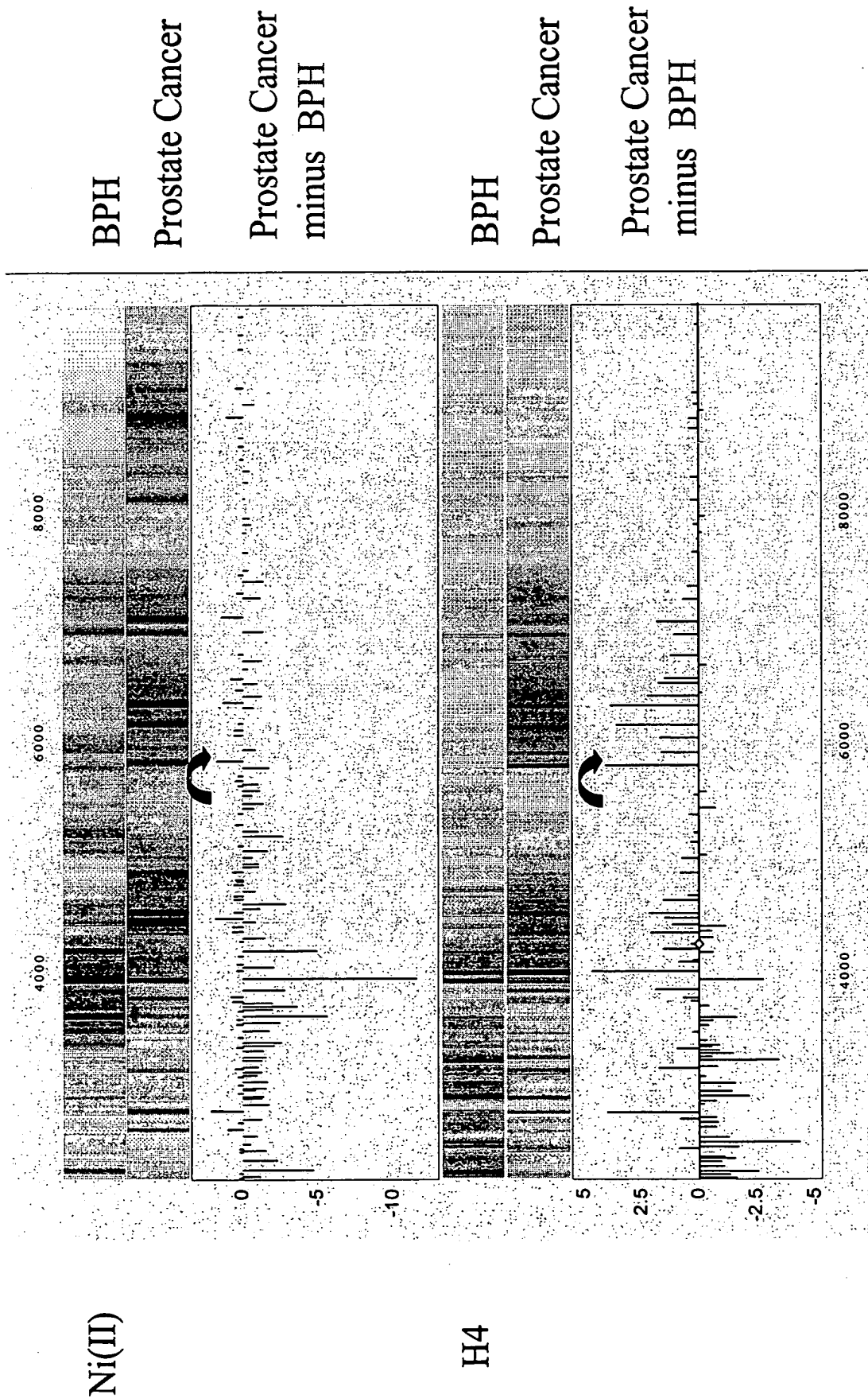


FIG. 3

20110101 165539001

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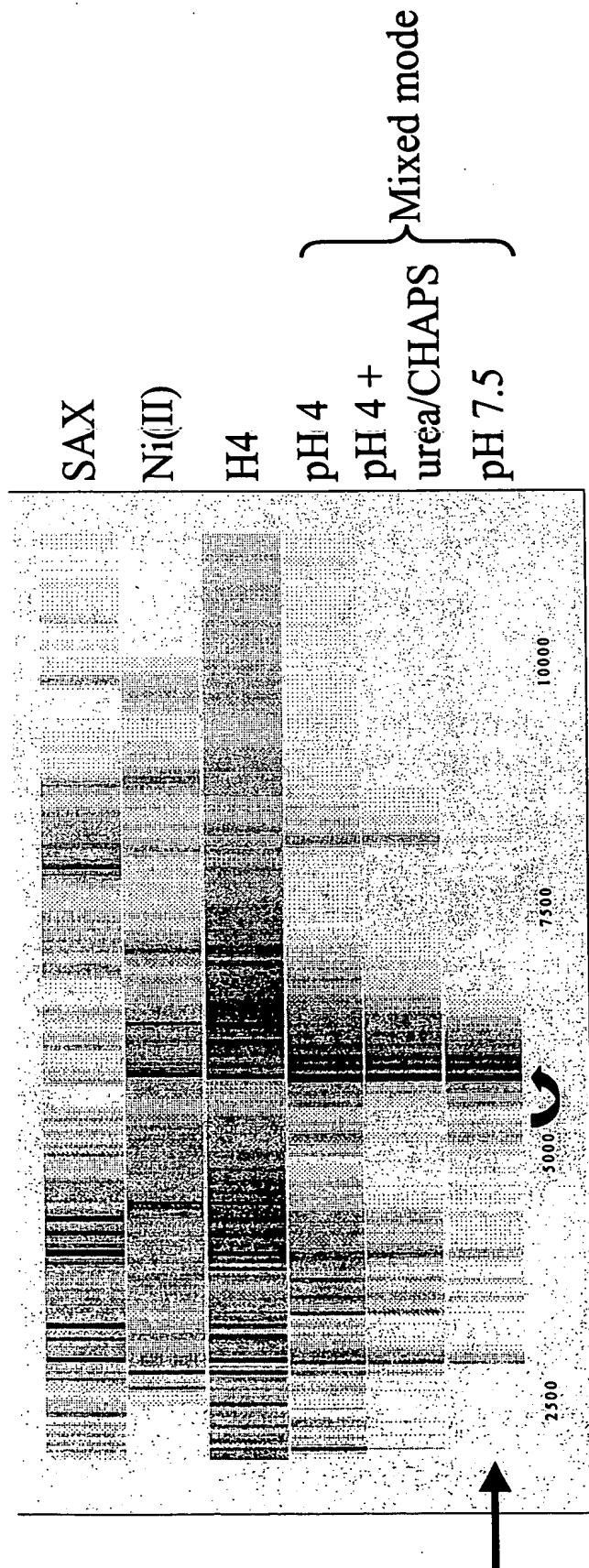


FIG. 4

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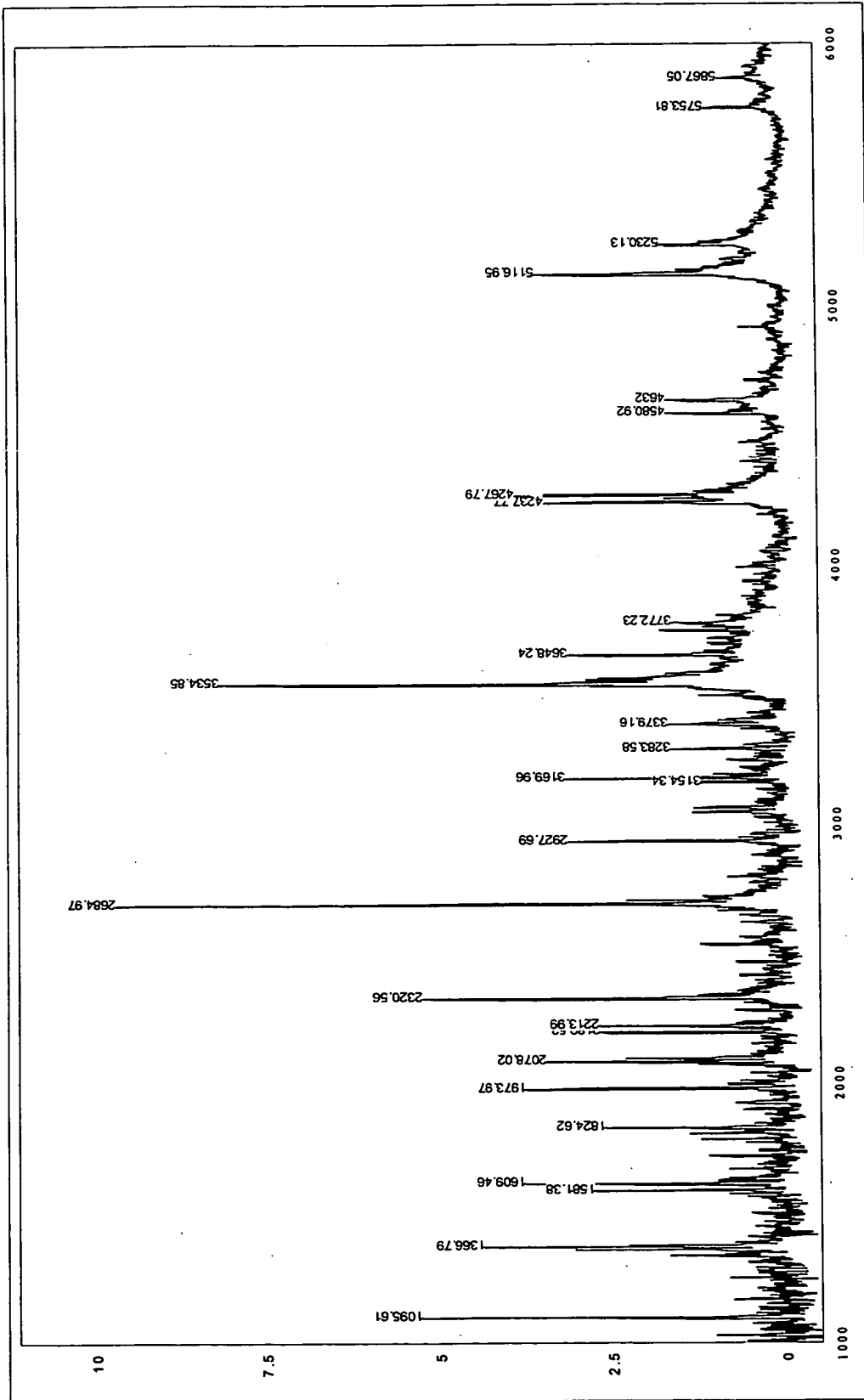


FIG. 5

10066359 "013102

Sheet 6 of 27

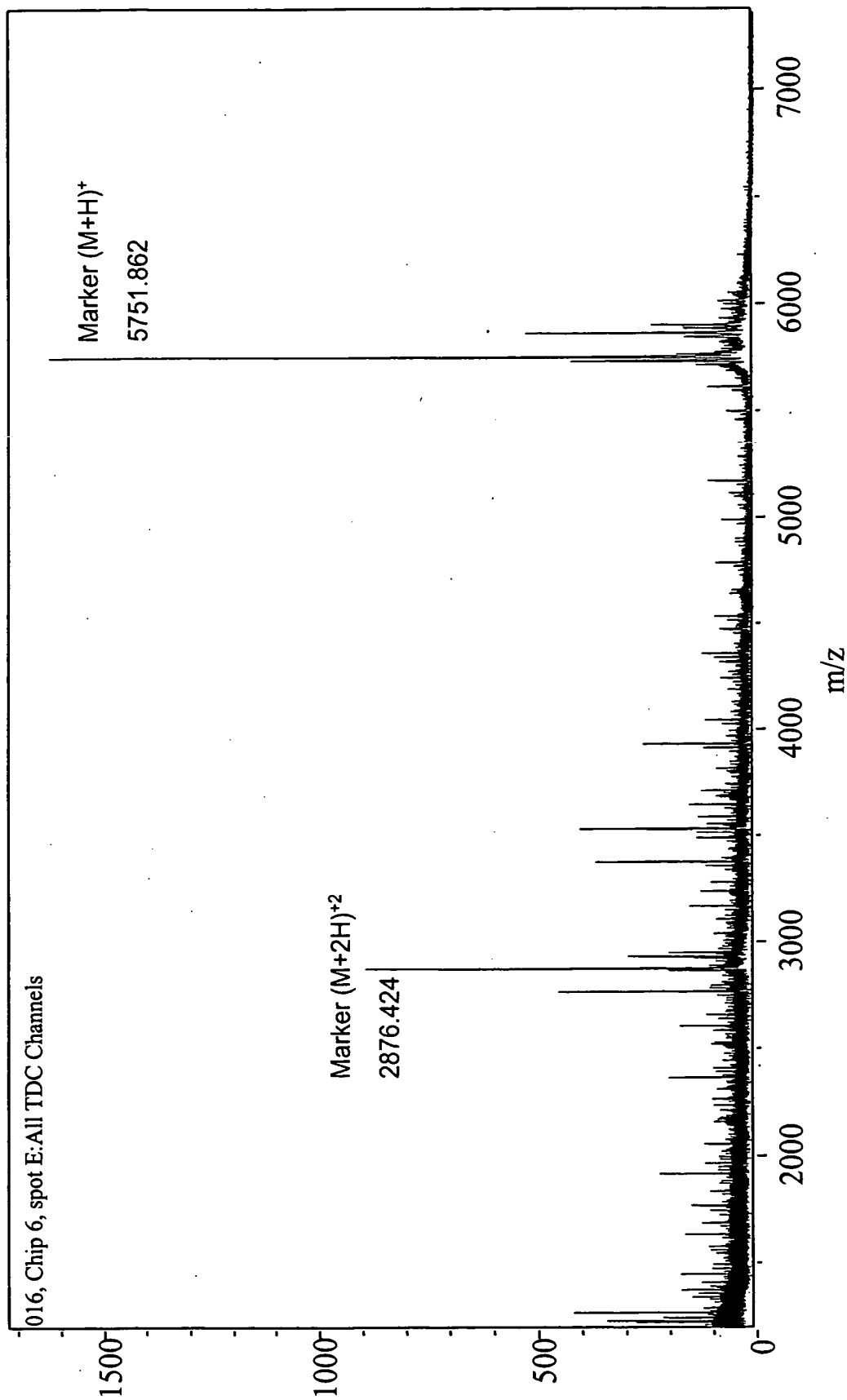


FIG. 6

20140606 09:00:00

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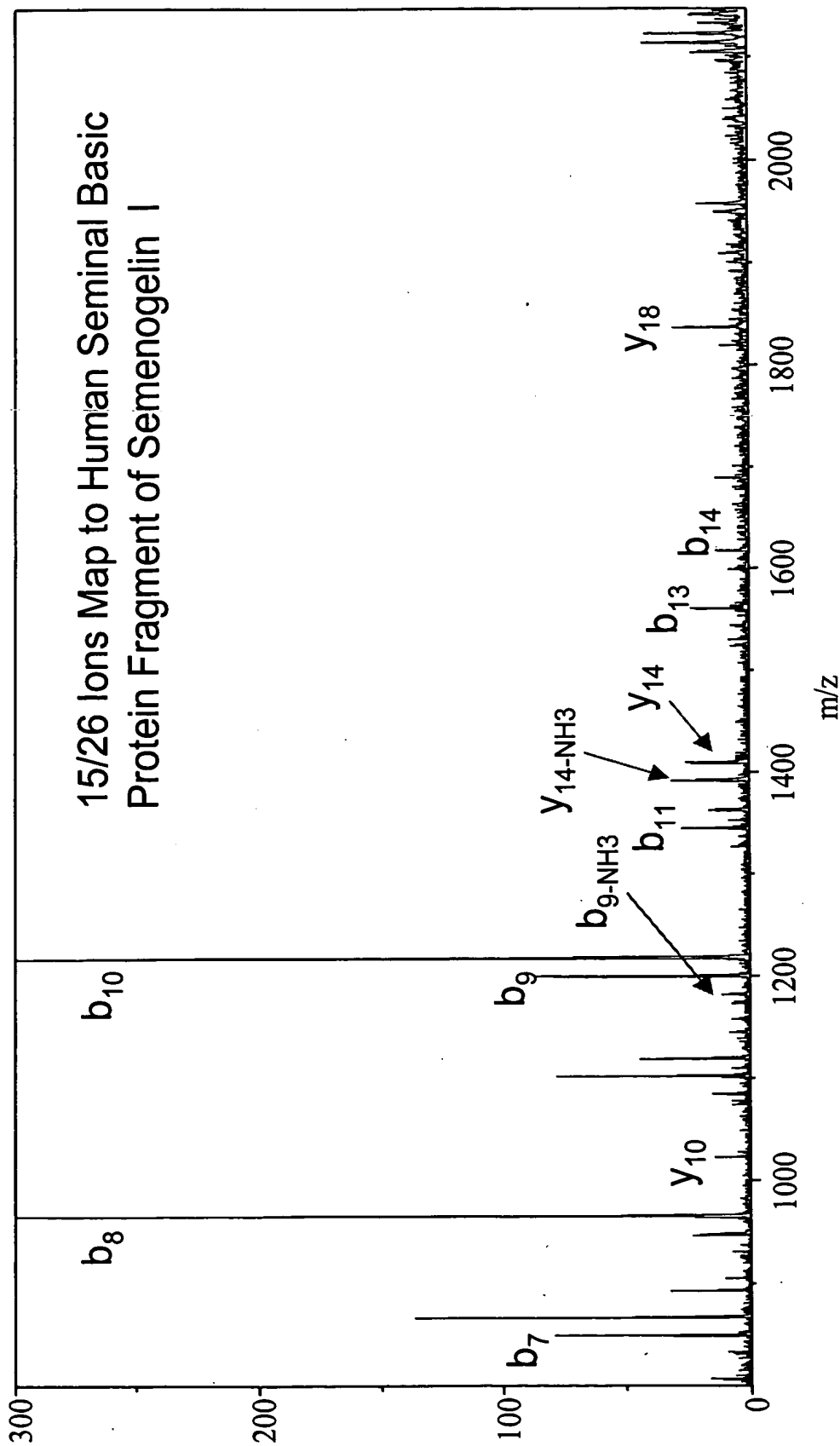


FIG. 7

Sheet 8 of 27

Retentate Mapping of a Peptide Map on a Reverse Phase ProteinChip® Array

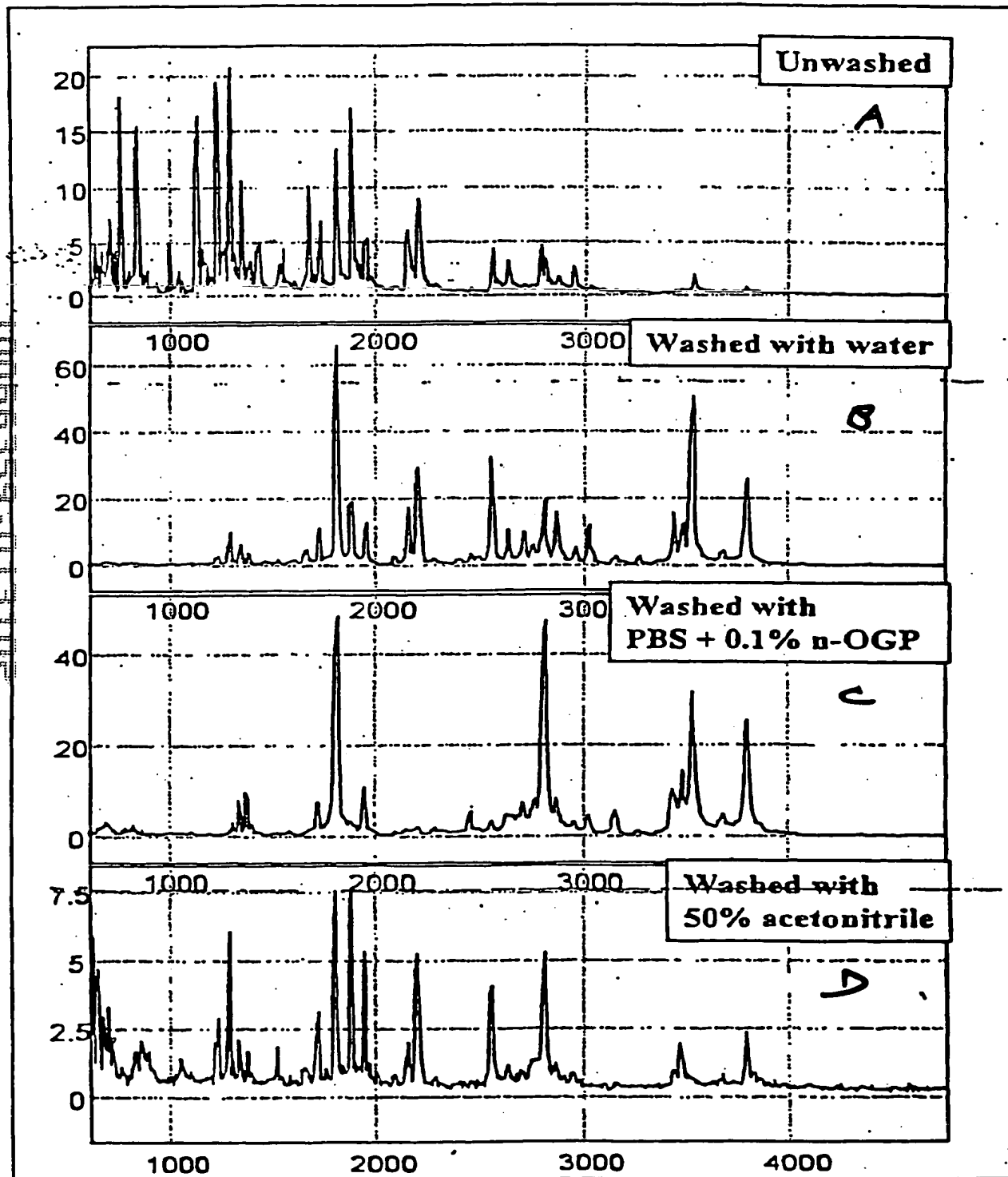


FIG. 8

Sheet 9 of 27

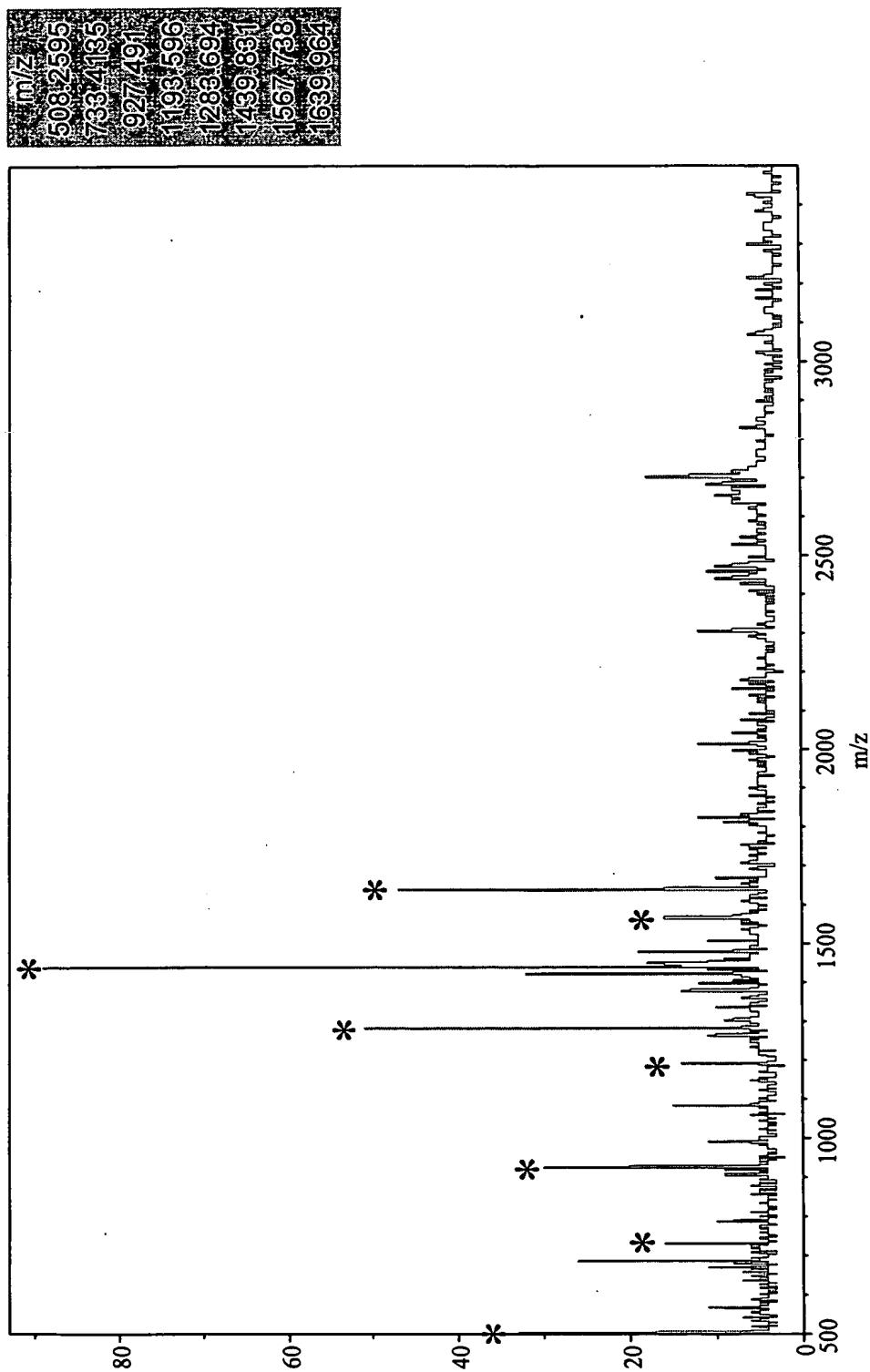


FIG. 9

Sheet 10 of 27

m/z
508.2488
572.3584
689.3708
733.4133
906.4743
927.4924
1001.583
1083.596
1193.603
1283.707
1439.806
1595.88
1639.933
1810.986
1823.904
1897.078

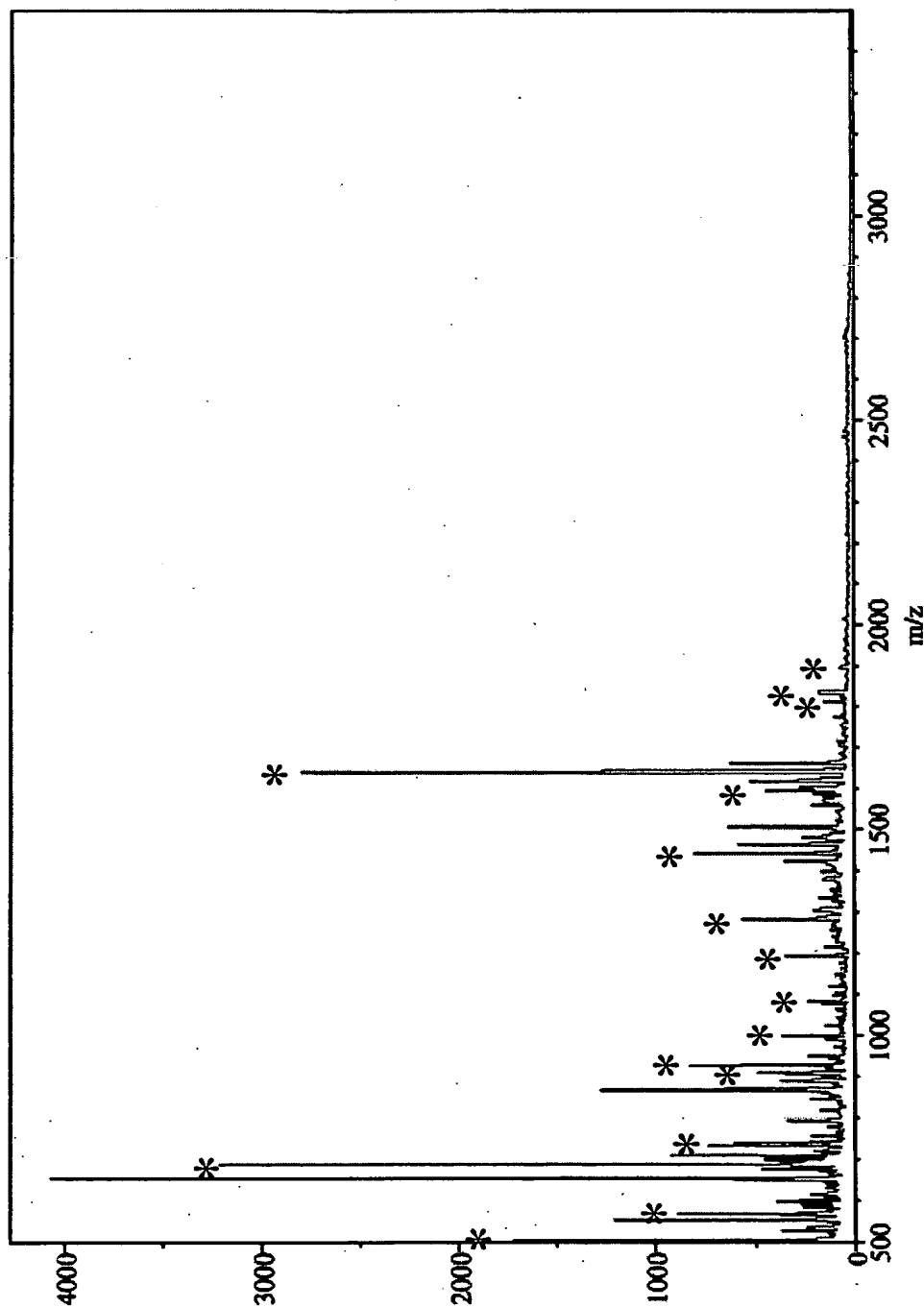


FIG. 10

20110101 655999001

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ragment esidues	Cal. M/Z	pI	H2O	pH3	pH4	pH5	pH6	pH7	pH8	pH9	All Conditions
30	204-207	K/F...R/A	508.2518	508.2524	508.2523	508.2507	508.2488	508.2477	508.2471	508.2471	508.2518
27-28	194-197	R/Q...R/C	572.3628	572.3636	572.3628	572.3623	572.3584	572.3585	572.3576	572.3581	572.3628
32	211-216	K/A...R/L	689.3728	689.3766	689.3753	689.3753	689.3708	689.3693	689.3692	689.37	689.3728
26	187-193	K/V...R/Q	733.4208	733.4199	733.421	733.4202	733.4133	733.4159	733.4093		733.4208
66	457-463	R/L...K/T	841.4598	847.5069	847.5087			847.5046		847.4989	841.4598
33-34	217-223	R/L...K/A	847.5038	906.4826	906.4814	906.4786	906.4743	906.4694			847.5038
24-25	180-186	K/L...K/V	906.4718	927.4975	927.497	927.4961	927.4924	927.4889	927.4886	927.4905	906.4718
28-29	196-203	R/L...K/F	918.5188	990.5469	990.5759						918.5188
19	137-143	K/Y...R/R	927.4938	1001.592	1001.592	1001.585	1001.583	1001.568	1001.568	1001.582	927.4938
25-26	185-193	R/E...R/Q	990.5578	1083.597	1083.602	1083.601	1083.596	1083.59	1083.605	1083.575	990.5578
31-32	208-216	R/A...R/L	1001.589	1193.603	1193.611	1193.595	1193.603	1193.596	1193.593	1193.6	1001.588
26-27	187-195	K/V...R/L	1017.58	1283.726	1283.714	1283.712	1283.707	1283.701	1283.697	1283.712	1017.58
69	473-481	K/C...R/R	1024.455	1305.707	1305.689	1305.693					1024.455
19-20	137-144	K/Y...R/H	1083.595	1439.812	1439.819	1439.812	1439.806	1439.801	1439.794	1439.81	1083.5948
29-30	198-207	R/C...R/A	1138.568	1585.906	1585.882	1585.891	1585.88	1585.88	1585.88	1585.895	1138.5678
36893	36901	-D...R/F	1193.602	1639.943	1639.944	1639.94	1639.933	1639.928	1639.928	1639.928	1193.6018
36854	37215	R/F...K/G	1249.621	1692.942	1692.942	1692.942	1692.942	1692.942	1692.942	1692.942	1249.6208
50	336-346	R/H...R/L	1283.711	1750.952	1750.961	1750.961	1750.961	1750.961	1750.961	1750.961	1283.7108
55	377-387	K/H...K/Z	1305.716	1811.009	1811.015	1811.035	1810.986	1811.007	1810.992	1811.008	1305.7158
8	65-76	K/S...K/V	1362.672	1823.912	1823.907	1823.9	1823.904	1823.904	1823.904	1823.8998	1362.6718
49-50	335-346	R/R...R/L	1439.812	1962.931	1962.931	1962.931	1962.931	1962.931	1962.931	1962.931	1439.8118
18-19	133-143	K/F...R/R	1445.758	2031.035	2031.035	2031.035	2031.035	2031.035	2031.035	2031.035	1445.758
68-70	470-482	K/V...R/P	1508.767	2157.157	2157.157	2157.157	2157.157	2157.157	2157.157	2157.157	1508.767
48	322-334	K/D...R/R	1567.743	2264.167	2264.167	2264.167	2264.167	2264.167	2264.167	2264.167	1567.743
50-51	336-349	R/H...K/E	1595.927	2411.1	2411.13	2411.13	2411.13	2411.13	2411.13	2411.13	1595.927
74-77	519-533	K/Q...K/P	1777.106	2557.157	2557.157	2557.157	2557.157	2557.157	2557.157	2557.157	1777.106
59-60	411-425	R/K...R/S	1639.938	2701.244	2701.244	2701.244	2701.244	2701.244	2701.244	2701.244	1639.938
65	443-456	R/M...R/L	1687.813	2857.157	2857.157	2857.157	2857.157	2857.157	2857.157	2857.157	1687.813
35-36	224-238	K/A...K/V	1692.942	2957.157	2957.157	2957.157	2957.157	2957.157	2957.157	2957.157	1692.942
33-35	217-231	R/L...K/L	1750.974	3057.157	3057.157	3057.157	3057.157	3057.157	3057.157	3057.157	1750.974
66-68	457-472	R/L...K/C	1811.009	3157.157	3157.157	3157.157	3157.157	3157.157	3157.157	3157.157	1811.009
70-71	482-497	R/R...K/A	1823.9	3257.157	3257.157	3257.157	3257.157	3257.157	3257.157	3257.157	1823.9
60-61	412-429	K/V...K/V	1897.075	3357.157	3357.157	3357.157	3357.157	3357.157	3357.157	3357.157	1897.075
14-16	115-131	K/L...K/K	1962.948	3457.157	3457.157	3457.157	3457.157	3457.157	3457.157	3457.157	1962.948
47-48	316-334	K/N...R/R	2301.082	3557.157	3557.157	3557.157	3557.157	3557.157	3557.157	3557.157	2301.082
36895	36911	-D...K/G	2424.205	3657.157	3657.157	3657.157	3657.157	3657.157	3657.157	3657.157	2424.205
37-39	239-260	K/V...K/Y	2441.1	3757.157	3757.157	3757.157	3757.157	3757.157	3757.157	3757.157	2441.1
47-49	316-335	K/N...R/H	2457.183	3857.157	3857.157	3857.157	3857.157	3857.157	3857.157	3857.157	2457.183
14-18	115-136	K/L...K/Y	2609.306	3957.157	3957.157	3957.157	3957.157	3957.157	3957.157	3957.157	2609.306
63-65	434-456	R/C...R/L	2701.245	4057.157	4057.157	4057.157	4057.157	4057.157	4057.157	4057.157	2701.245
36-39	232-260	K/L...K/Y	3211.554	4157.157	4157.157	4157.157	4157.157	4157.157	4157.157	4157.157	3211.554
51-54	347-376	R/L...K/H	3420.579	4257.157	4257.157	4257.157	4257.157	4257.157	4257.157	4257.157	3420.579

Total Peptides
Sequence Coverage (%)

34
45

FIG. 11

Fragment	Residues	Cal. M/Z	pI	pH2	pH3	pH4	pH5	pH6	pH7	pH8	pH9	All Conditions
30	204-207	KF...RA	508.2518	6	508.2502	508.2478	508.2457	508.2456	508.2476	508.2478	508.2456	508.2518
27-28	194-197	R/Q...RC	572.3628	12	572.3639	572.3529	572.352	572.3545	572.3527	572.3529	572.3527	572.3628
32	211-216	K/A...RL	689.3728	9.8	689.371	689.3697	689.3668	689.3668	689.3702	689.3701	689.3629	689.3728
26	187-193	KV...R/Q	733.4208	9.7	733.4115	733.4089	733.4003					733.4208
66	457-463	RL...K/T	841.4598	6.7								
33-34	217-223	RL...K/A	847.5038	10	906.4668	906.4671	906.4667	906.4706	906.4697	906.464	906.4672	906.4718
24-25	180-186	KL...KV	908.4718	6.1								
28-29	196-203	RL...K/F	918.5188	9.5	927.483	927.4887	927.4859	927.4861	927.4902	927.4927	927.4855	927.4938
19	137-143	KV...R/R	927.4938	6	1001.578	1001.582	1001.566		1001.571			1001.5888
25-26	185-193	R/E...R/Q	990.5578	8.8								
31-32	208-216	R/A...RL	1001.589	11								
26-27	187-195	KV...RL	1017.58	12	1024.445	1024.445	1024.446					
69	473-481	K/C...R/R	1024.455	6	1083.593	1083.593	1083.591	1083.588	1083.584	1083.593	1083.581	1024.4548
19-20	137-144	K/Y...R/H	1083.595	8.6								
29-30	198-207	R/C...R/A	1138.568	8.2	1193.605	1193.598	1193.596	1193.594	1193.599	1193.599	1193.596	1193.6018
36893	36901	-D...R/F	1193.602	6.9	1249.62	1249.62	1249.62	1249.605	1249.605	1249.605	1249.607	1249.6208
36954	37215	R/F...K/G	1249.621	5.4	1283.706	1283.7	1283.678	1283.694	1283.687	1283.702	1283.693	1283.7108
50	336-346	R/H...RL	1283.711	6.7	1305.704	1305.704						1305.7158
55	377-387	K/H...K/Z	1305.716	5.3	1439.808	1439.801	1439.795	1439.795	1439.797	1439.799	1439.792	1439.8118
8	65-76	K/S...K/V	1362.672	5.3								
49-50	335-346	R/R...RL	1439.812	8.7	1567.743	1567.74	1567.735	1567.751	1567.751	1567.731	1567.732	1567.7428
18-19	133-143	K/F...R/R	1445.758	8.5	1595.906	1595.906	1595.886	1595.885	1595.885	1595.882	1595.906	1595.9288
68-70	470-482	K/D...R/P	1508.767	10.8	1639.935	1639.928	1639.923	1639.923	1639.933	1639.934	1639.942	1639.9378
48	322-334	K/D...R/R	1567.743	4.4	1692.964	1692.964						1692.9418
50-51	336-349	R/H...K/E	1595.927	8.6	1810.957	1810.957	1810.998	1810.98	1810.989	1810.991		1811.0088
74-77	519-533	K/Q...K/P	1777.106	10	1823.885	1823.885						1823.8998
59-60	411-425	R/K...R/S	1639.938	8.7	1862.954	1862.954						1862.9478
65	443-456	R/M...RL	1667.813	4.4	2301.075	2301.075						2301.0818
35-36	224-238	K/A...K/V	1692.942	4.7	2424.192	2424.192						2424.2048
33-35	217-231	RL...K/L	1750.974	8.5								2441.0998
66-68	457-472	RL...K/C	1811.009	8.2								
70-71	482-497	R/R...K/A	1823.9	6								
60-61	412-429	KV...K/V	1897.075	8.7								
14-16	115-131	KL...K/K	1962.948	4.4								
47-48	316-334	KN...R/R	2301.082	4.7								
36895	36911	-D...K/G	2424.205	6.3								
37-39	239-260	KV...K/Y	2441.1	4.9								
47-49	316-335	K/N...R/H	2457.183	6.1								
14-18	115-136	KL...K/Y	2609.306	6.2								
63-65	434-456	R/C...RL	2701.245	4.9								
36-39	232-260	KL...K/Y	3211.554	4.9								
51-54	347-376	RL...K/H	3420.579	4.7								

Total Peptides
Sequence Coverage (%)

FIG. 12

26
37

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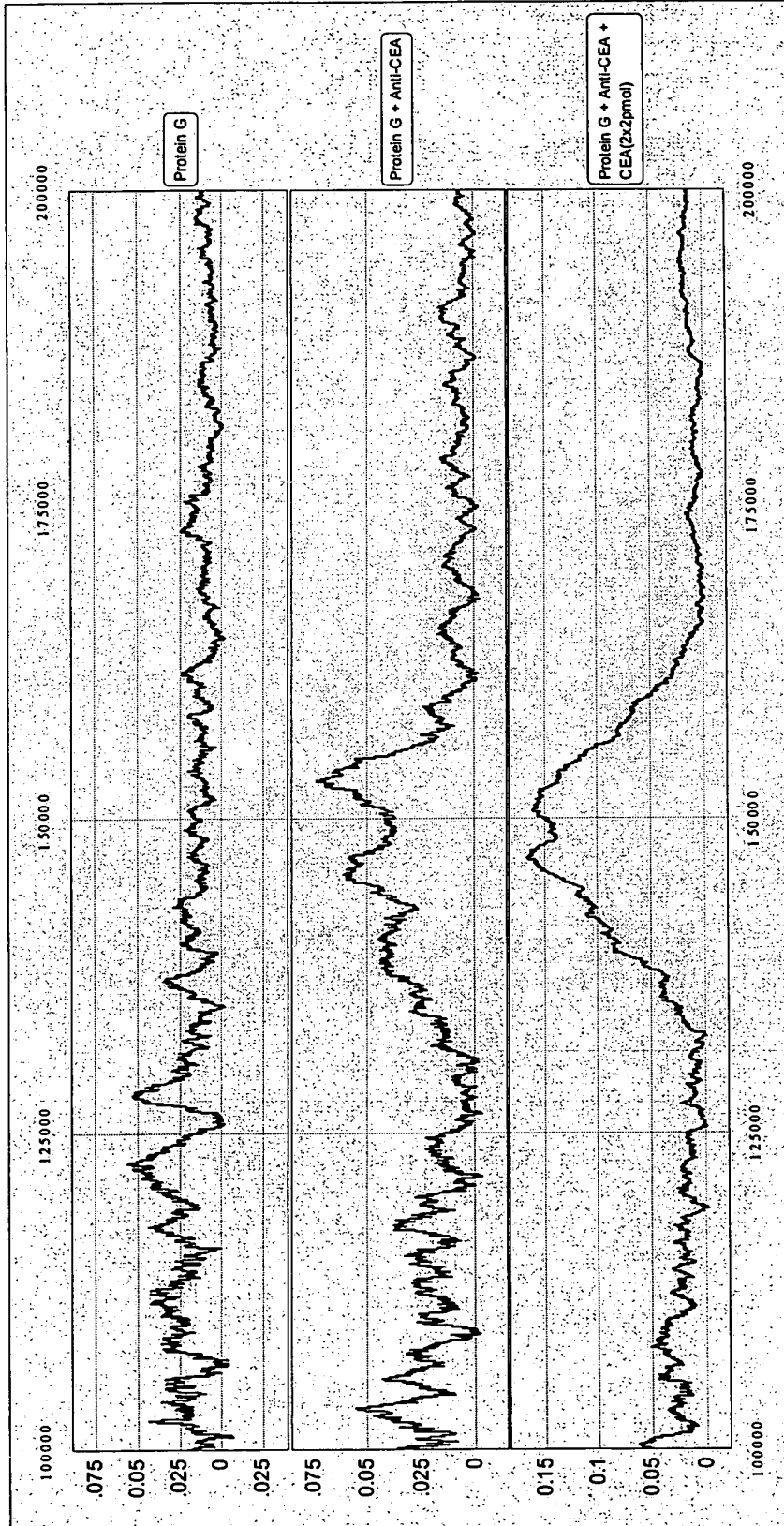


FIG. 13

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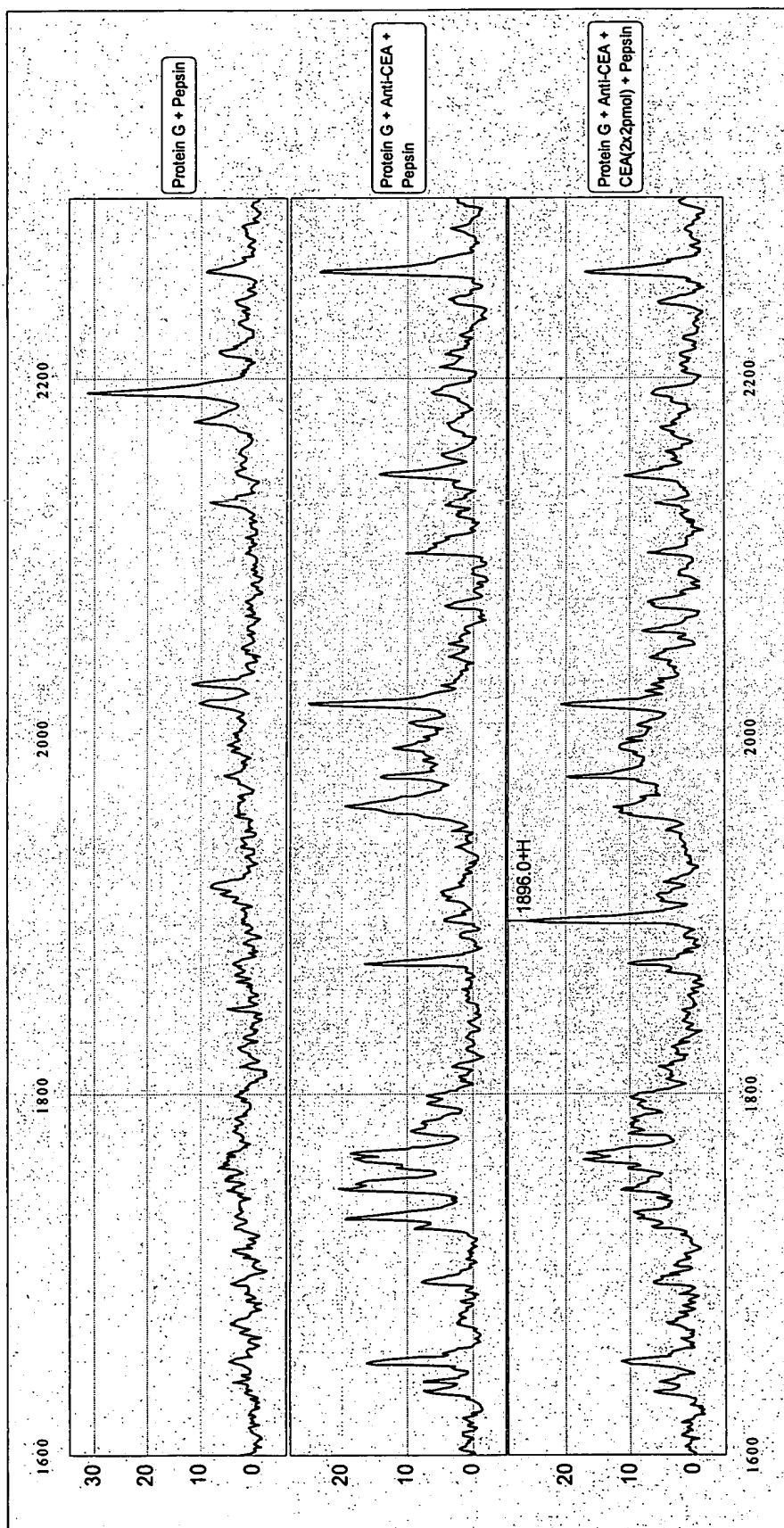


FIG. 14

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YVIGTQQATAYSGREPGP

Parent MH⁺
1894.9299

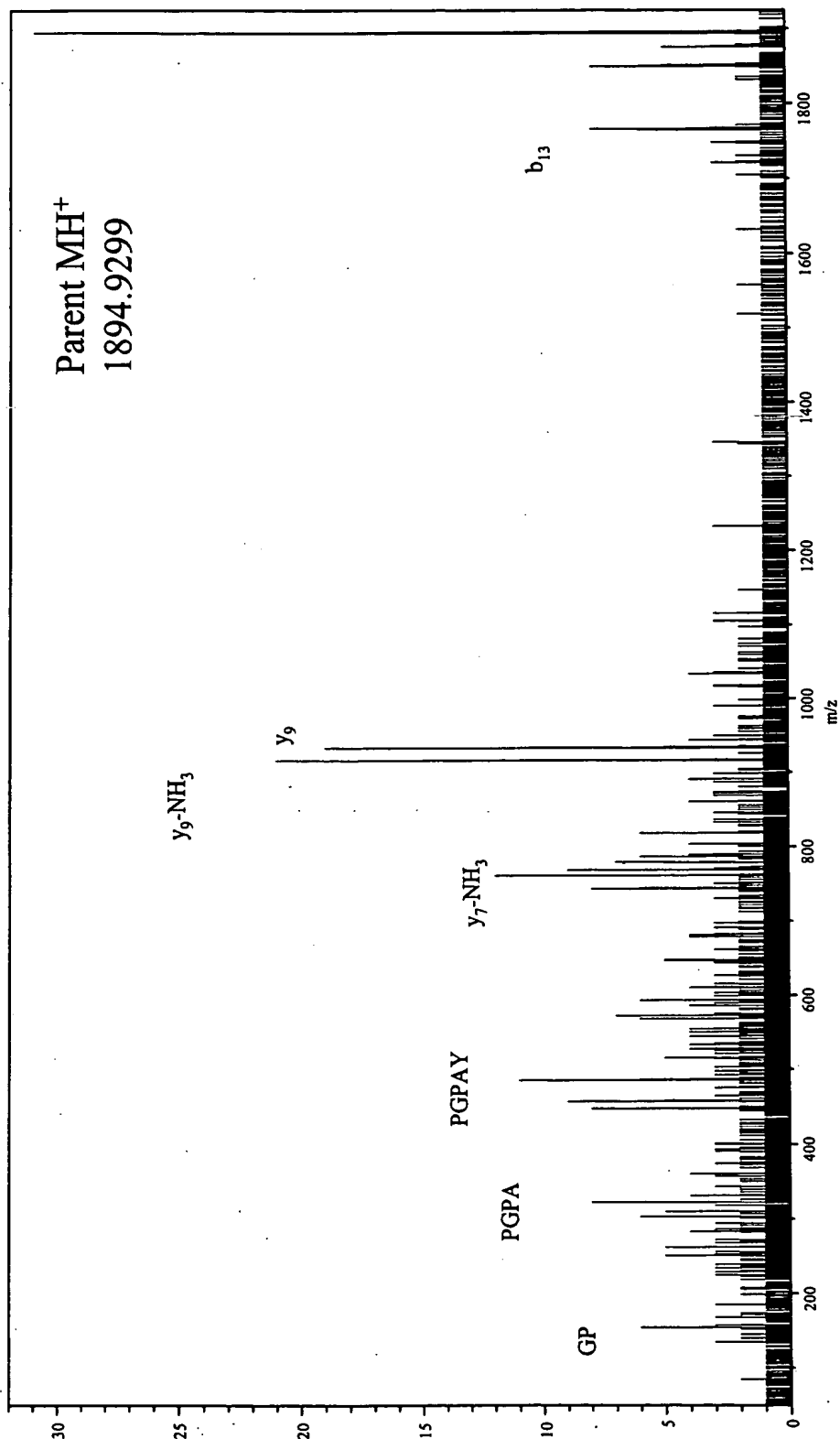


FIG. 15

20160630 09:00:00

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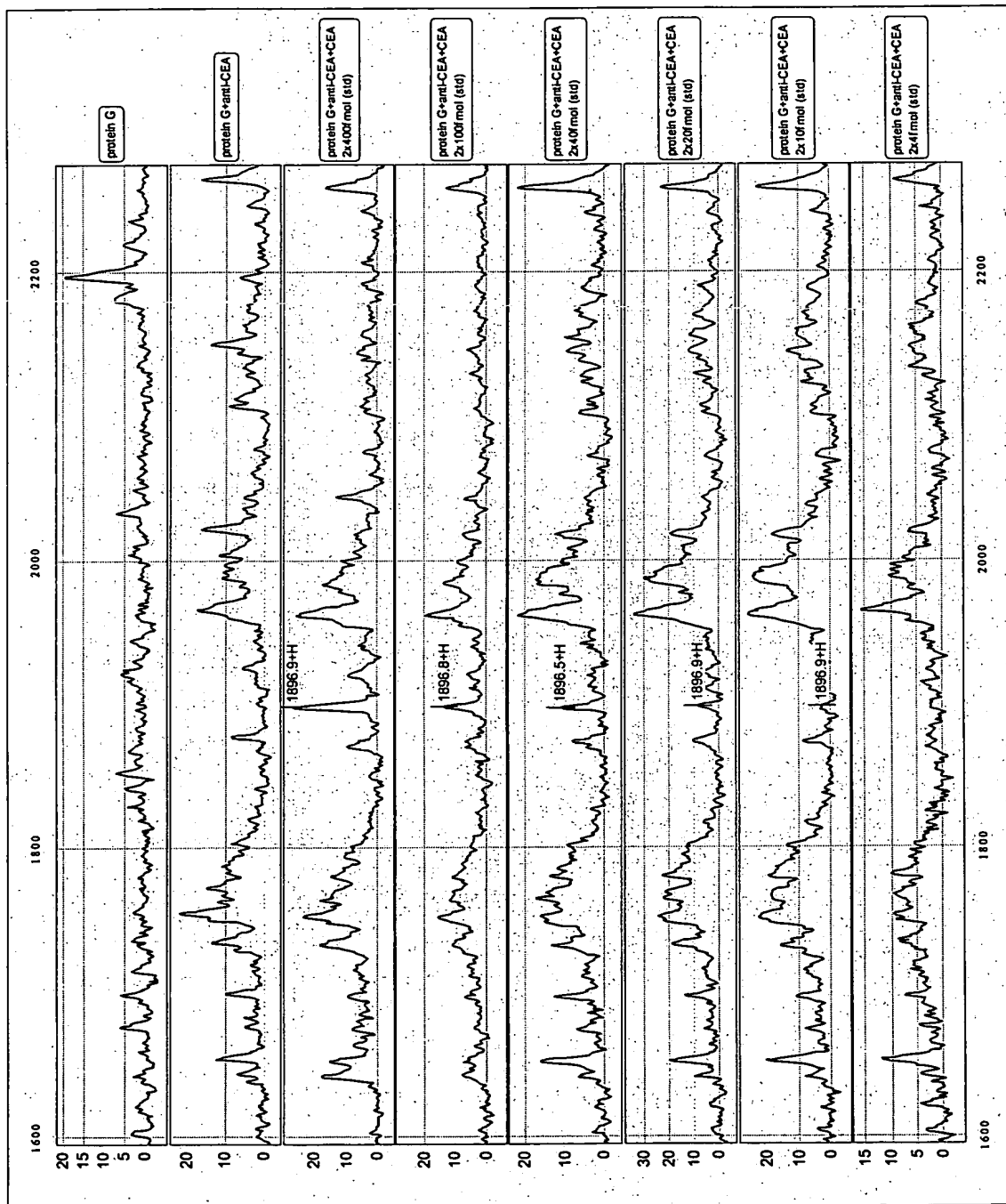


FIG. 16

Quantitative Antigen Capture

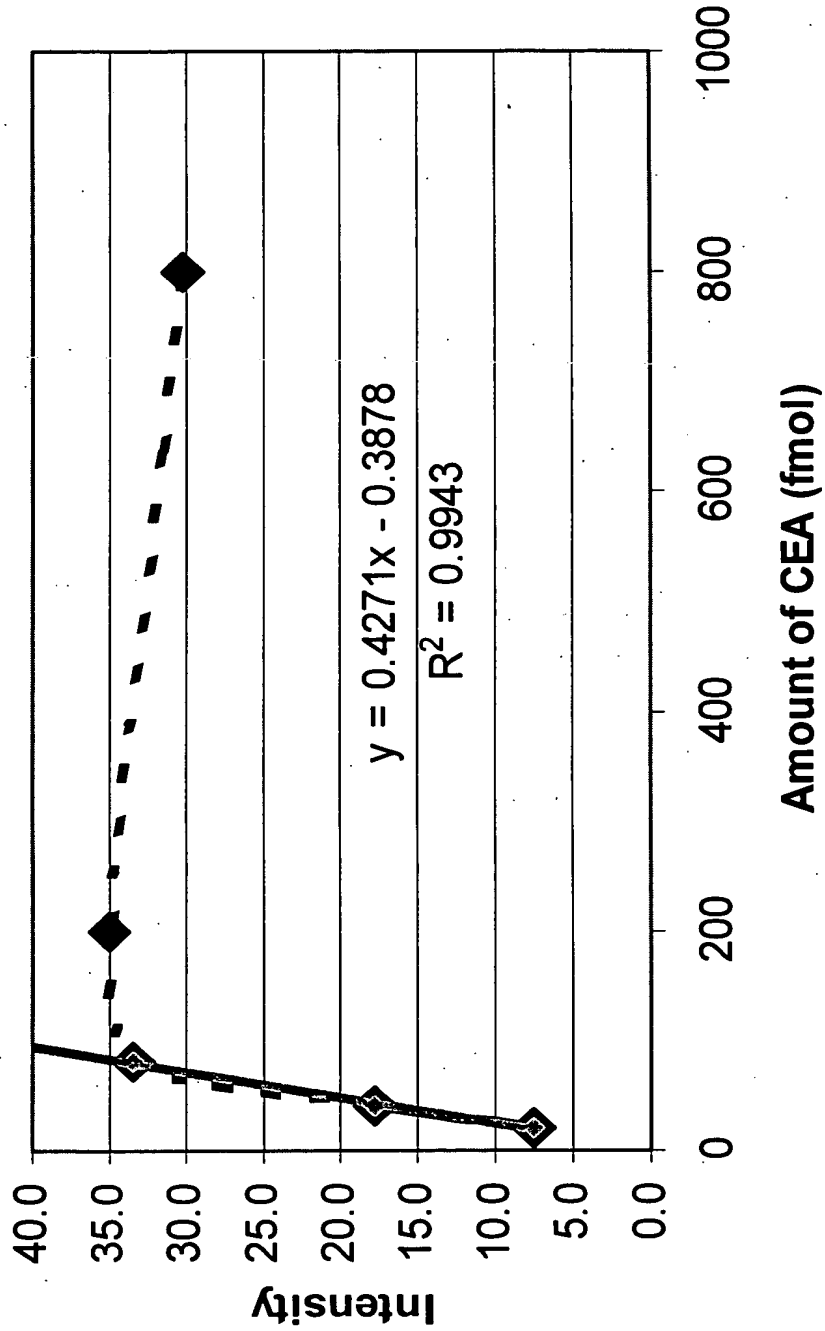


FIG. 17

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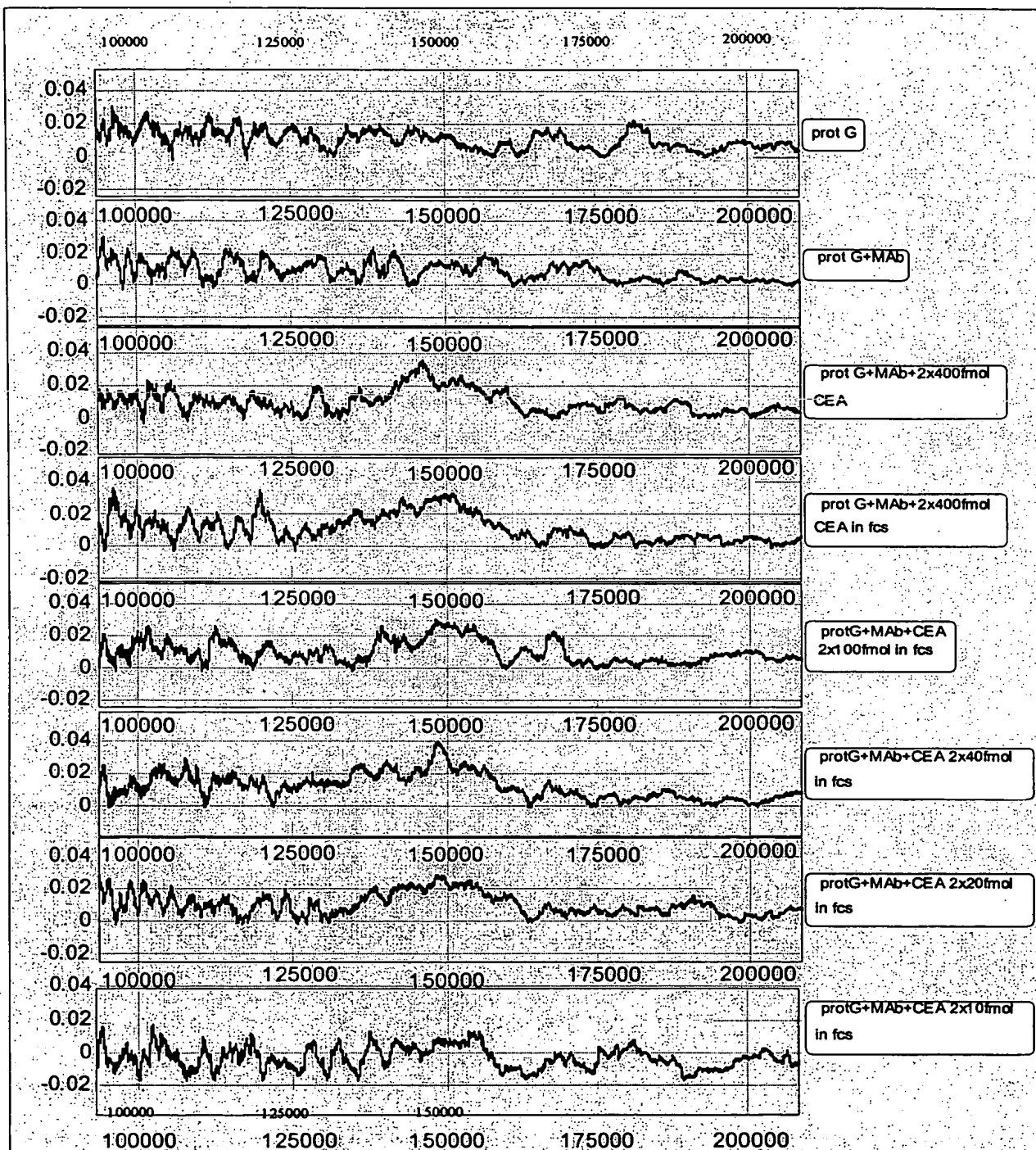


FIG. 18

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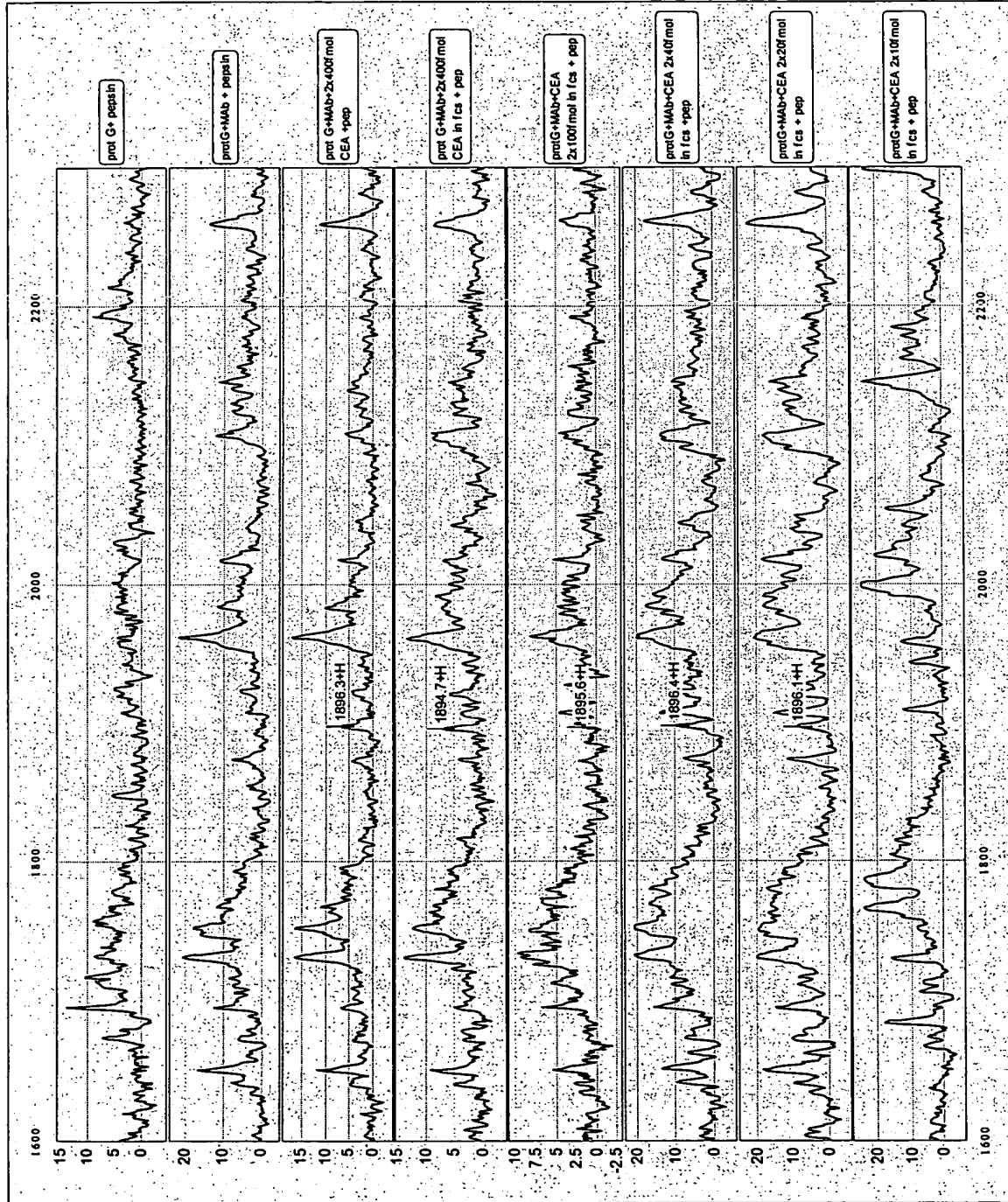


FIG. 19

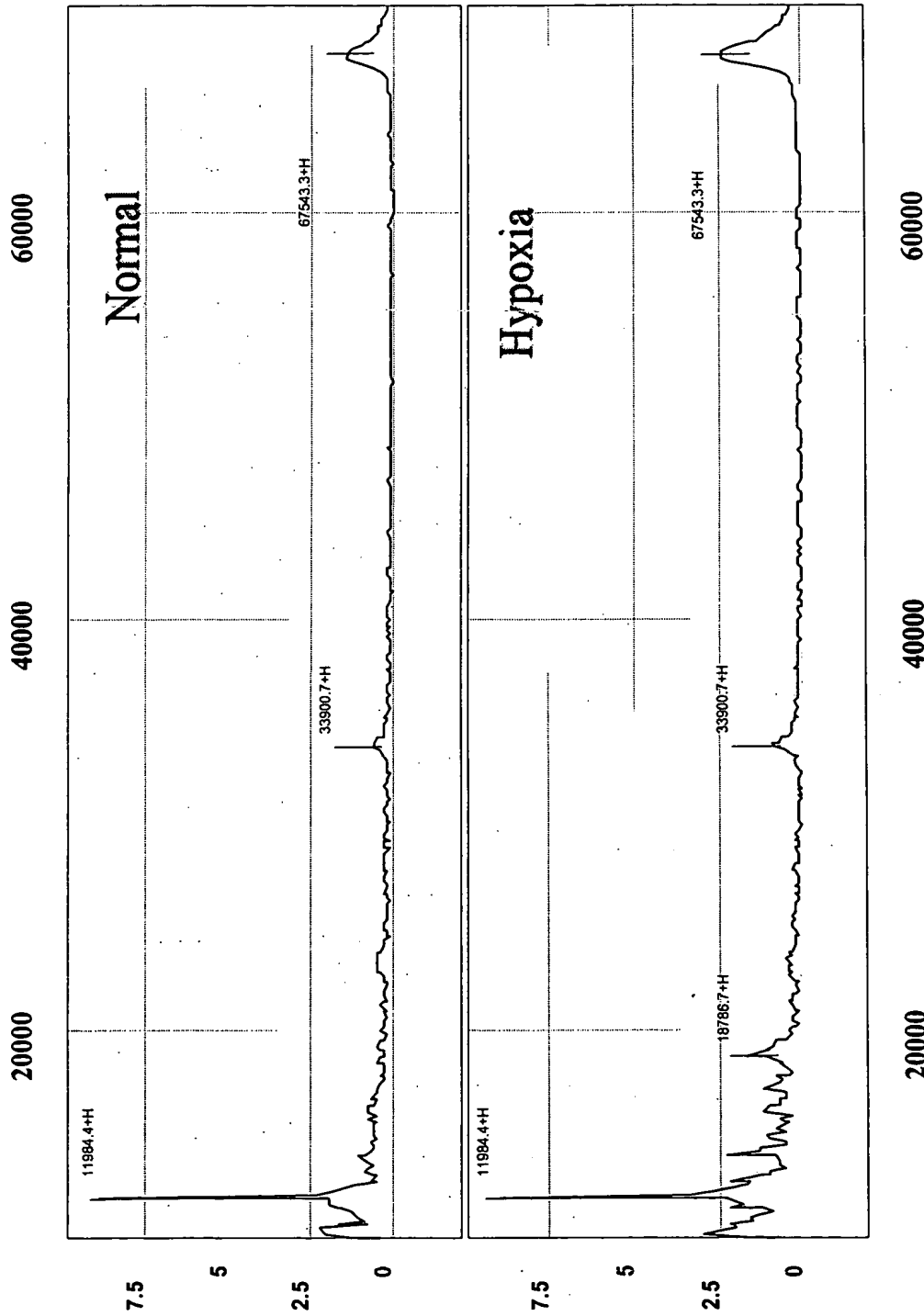
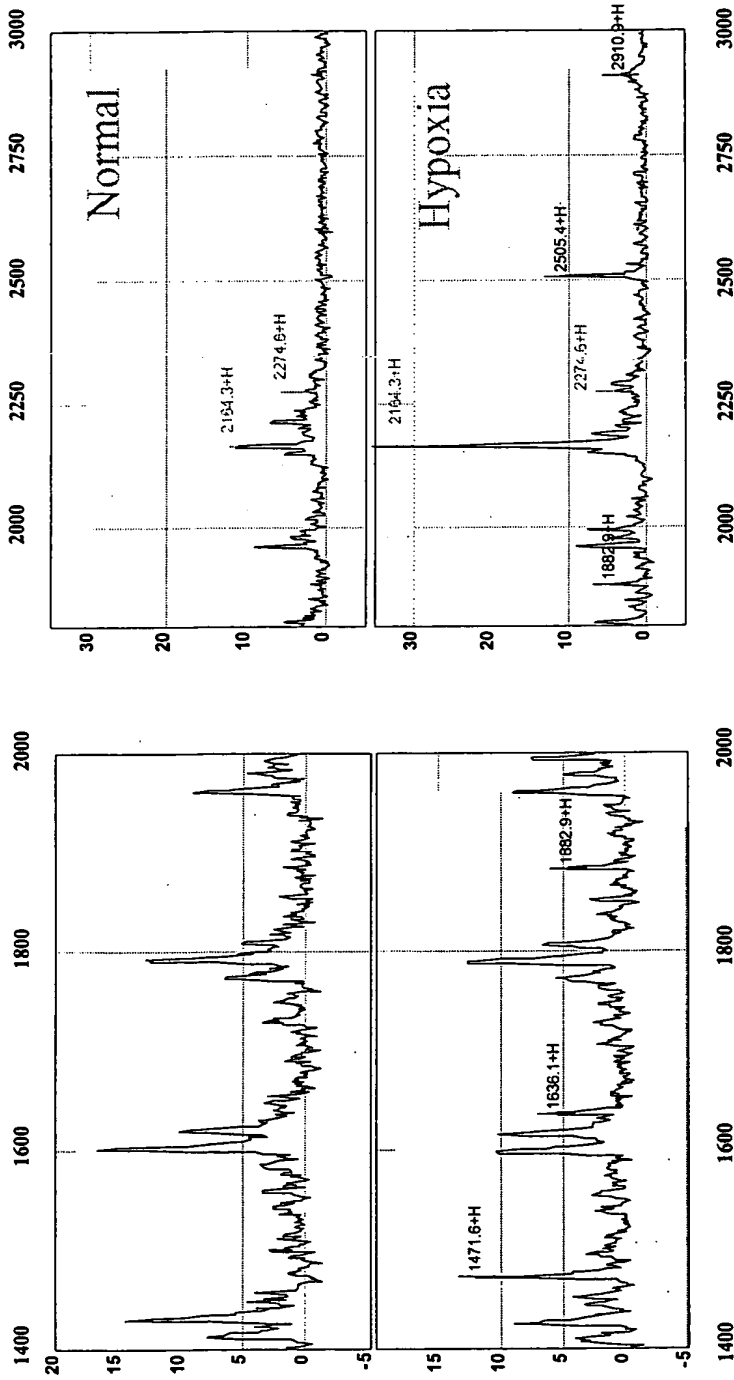


FIG. 20

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Fragments generated from trypsin autolysis: 2164.3, 2274.6

FIG. 21

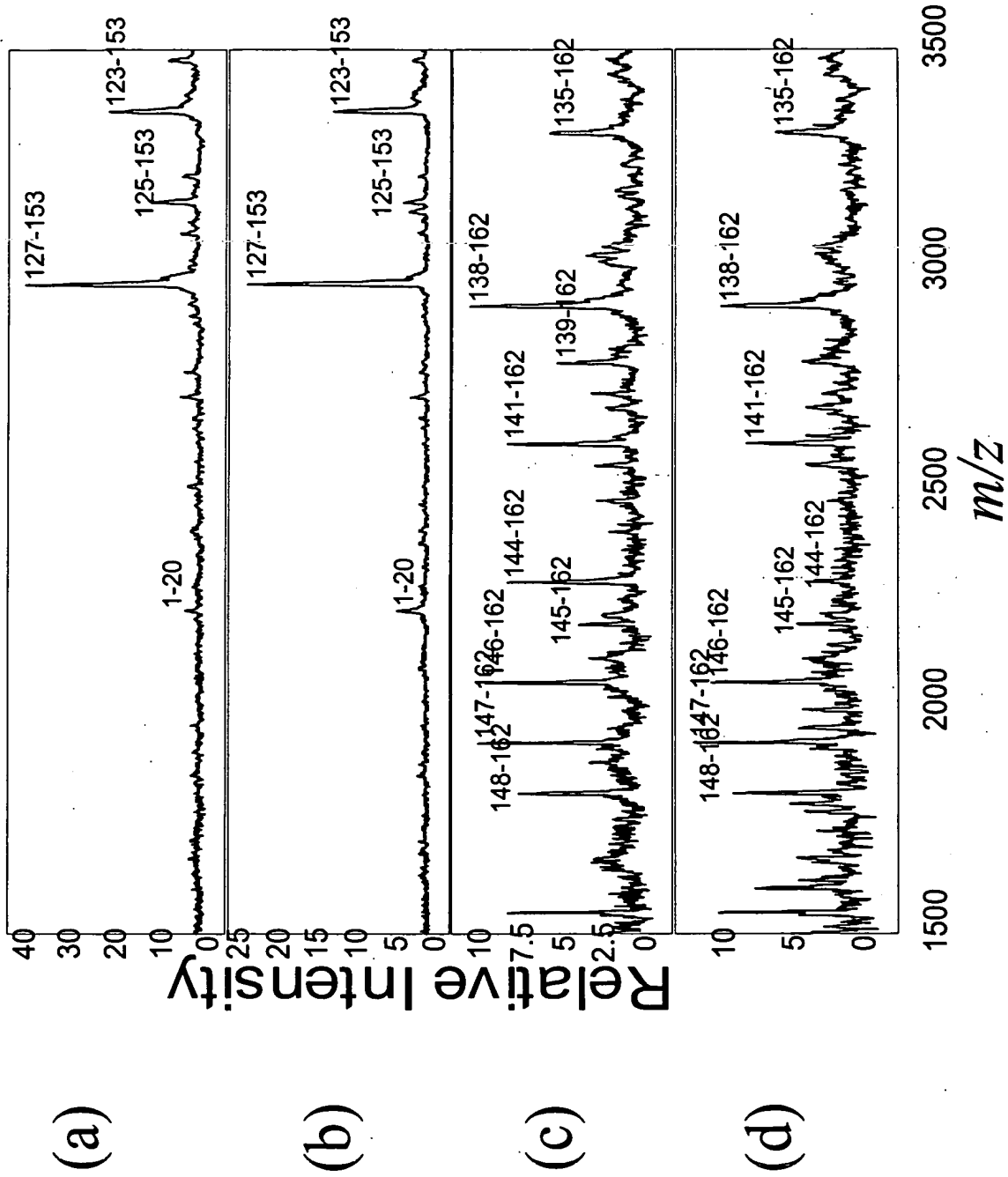


FIG. 22

2010-05-09

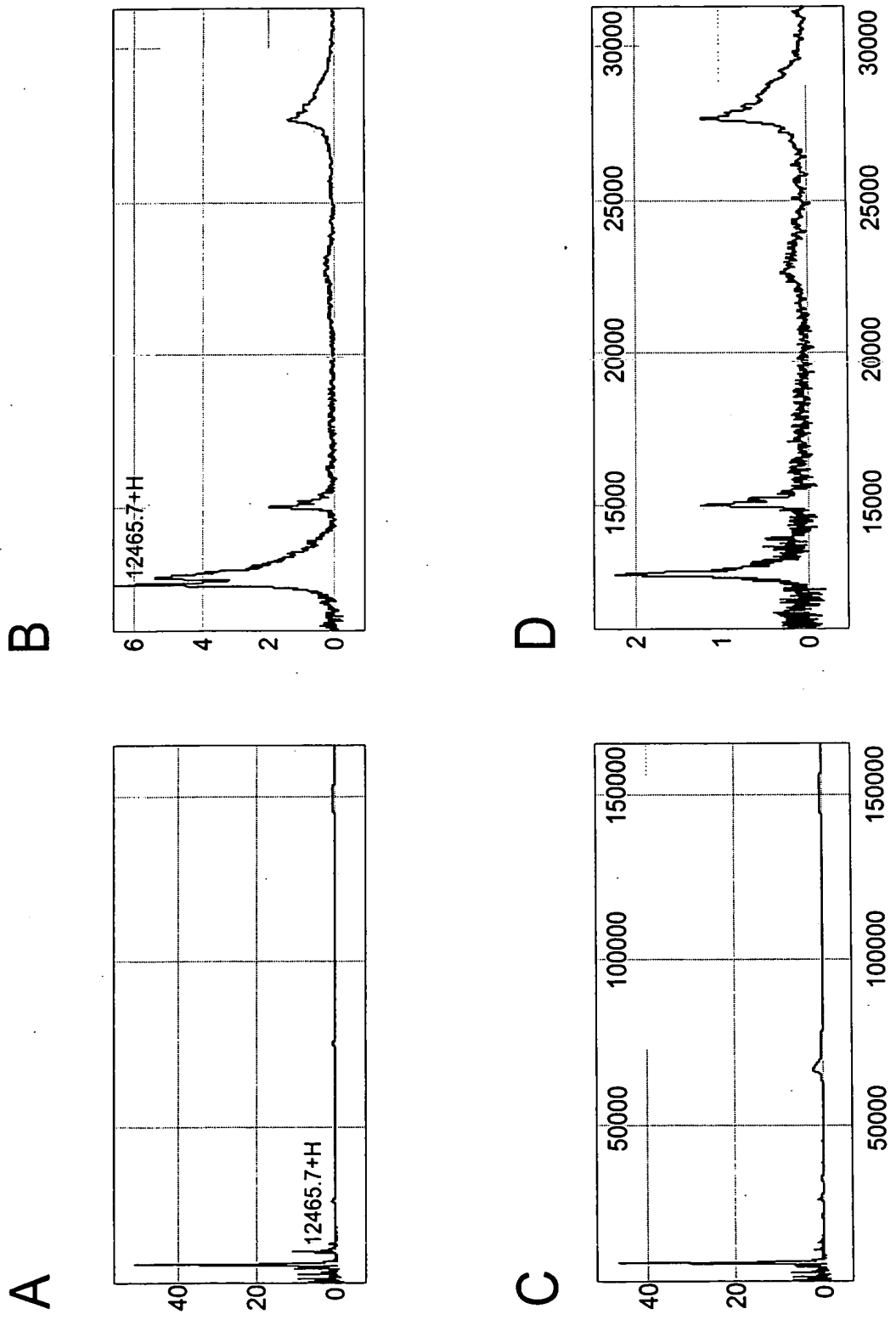
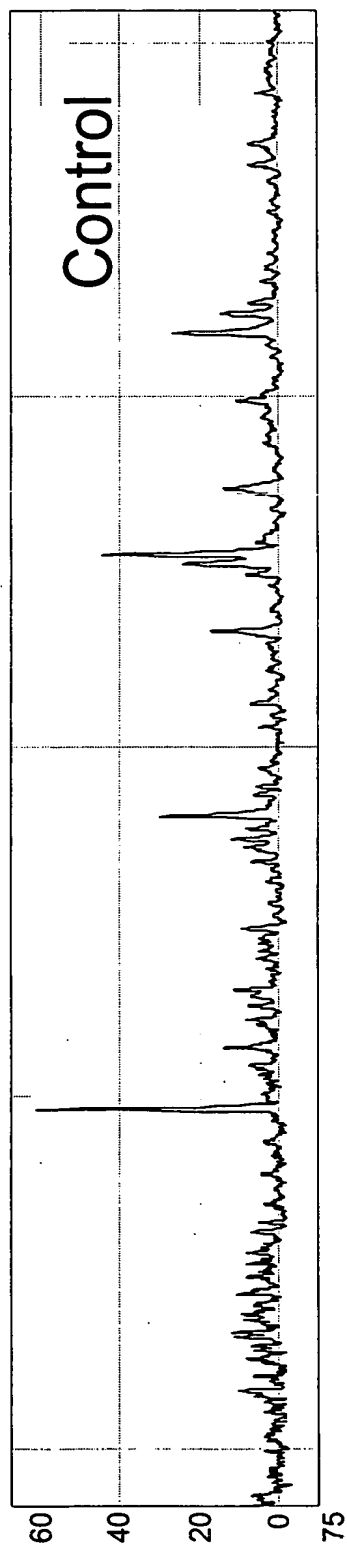


FIG. 23

Single MS



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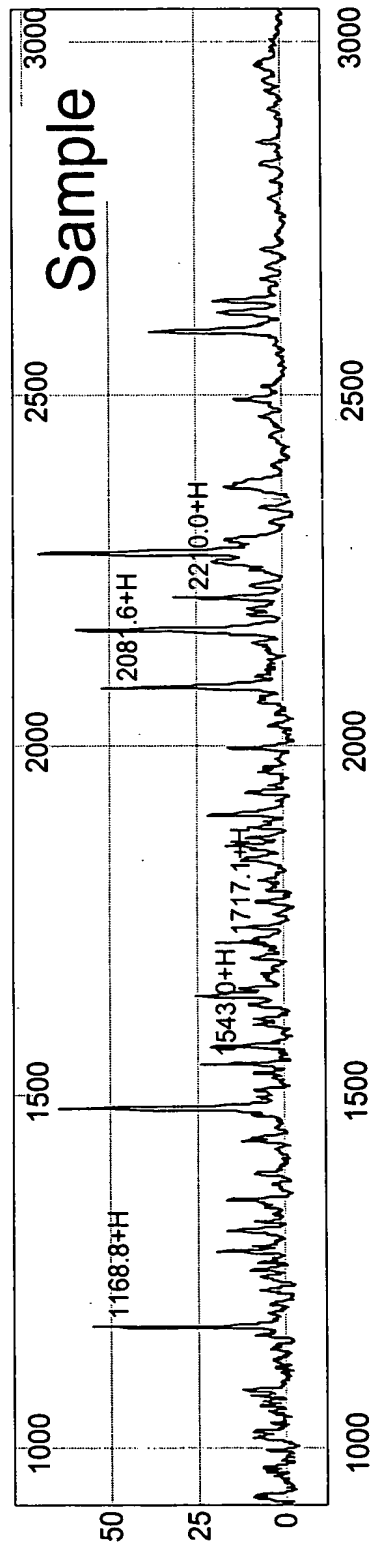
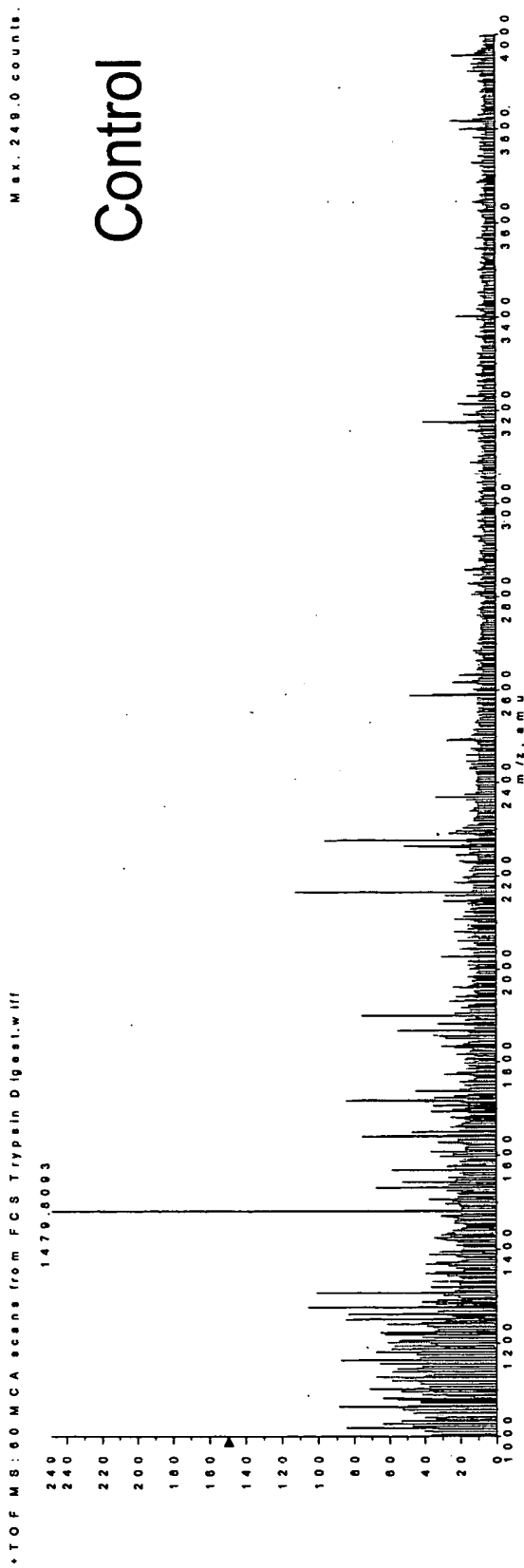


FIG. 24

201E10-65E99001

QqTOF Tandem MS

A



B

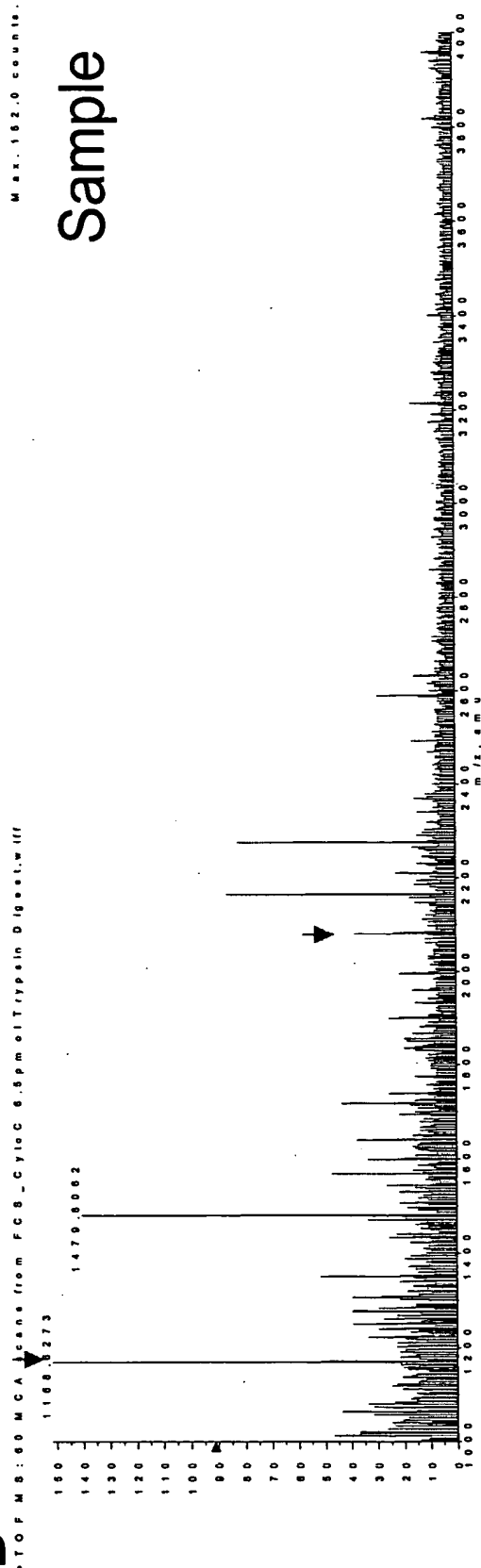


FIG. 25

20131016 09001

1168 MS/MS

+TOF Product (1168.0): 97 MCA scans from FCS_CytoC 6.5pmol Trypsin Digest 1168MSMS.wiff

Max. 148.0 counts.

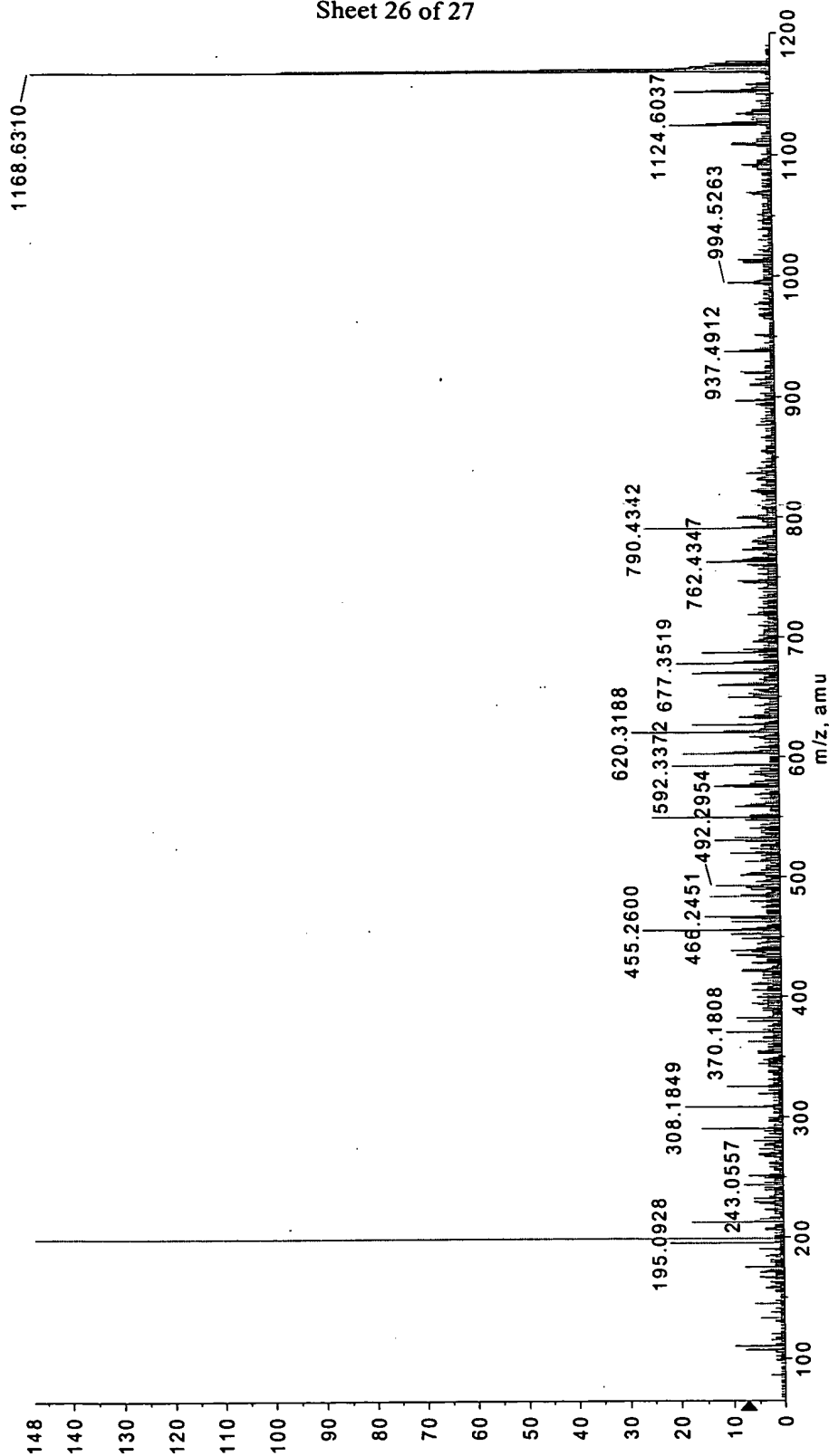


FIG. 26

Sheet 27 of 27

MS-Tag Search Results

Press stop on your browser if you wish to abort this MS-Tag search prematurely

Sample ID (Comment): Apo A-11040/ AKPVEDLR

Database searched: NCBInr 12.5.2001

Full Molecular Weight range: 810480 entries

Full pI range: 810480 entries

Presearch select: 810480 entries

Ion Types Considered: a-NH3⁺ b-H2O b-H2O y-NH3⁺ y-H2O x-H₂O

Search Peptide Masses: Digest: Max # Missed: Cysteines: Peptide
 Mode are Used: Cleavages: Modified by: N-terminus: C-terminus:
 identity: monoisotopic: Trypsin: 3: unmodified: Hydrogen (H): Free Acid (OH)

Number of sequences passing through parent mass filter: 18097

MS-Tag search select: 33 entries (results displayed for top 25 matches)

Parent mass: 11686310 (+/- 50.0000 ppm)

14 Fragment ions used in search: 175.10, 195.09, 243.06, 308.18, 455.26, 549.31, 620.32, 669.35, 677.35, 762.43, 780.43, 937.49, 994.53, 1108.60 (+/- 50.00 ppm)

Max # Unmatched Ions = 7

Result Summary

Rank	Unmatched Ions	Sequence	MH ⁺ Calculated Error (Da)	MH ⁺ Protein MW (Da)	Species	NCBI Inr 12.5.2001 Accession #	Protein Name
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	71110808.9/9.63	HOMO SAPIENS	15979398	(BC015130) cytochrome c
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	71110888.0/9.52	UNREADABLE	14782885	>gi14782885ref XP_043240.1 QXM_043240 hypothetical protein XP_043240 Homo sapiens]
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	71110757.8/9.59	UNREADABLE	4139715	>gi4139715pdb 1GIW Solution Structure Of Reduced Horse Heart Cytochrome C Nmr. Minimized Average Structure.
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	71110703.6/9.47	CHICKENS: HEART PEPTIDE 1047AA	914118	apocytochrome c
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	71110825.8/9.54	HORSES: HEART PEPTIDE 1047AA	914117	apocytochrome c
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	711108148.9/9.59	UNREADABLE	4139756	>gi4139756pdb WELF Cham H. Legel Fab Fragment Of E8 Antibody Complexed With Horse Cytochrome C At 1.8 A Resolution
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	711114743.9/61	GUINEA PIG TENTATIVE SEQUENCE	483111	cytochrome c

FIG. 27